

#5

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 101 S 32,395

Source: PCT

Date Processed by STIC: 4-29-05

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PCT

RAW SEQUENCE LISTING

DATE: 04/29/2005

PATENT APPLICATION: US/10/532,395

TIME: 17:00:36

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\04292005\J532395.raw

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3 <110> APPLICANT: University of Pennsylvania
4     Avarbock, David
5     Rubin, Harvey
6     Avarbock, Andrew
8 <120> TITLE OF INVENTION: Fragments and Activity of Rel protein in M. Tuberculosis and
other uses
9     thereof
W--> 10 <130> FILE REFERENCE: UPFT0002-100
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/532,395
C--> 12 <141> CURRENT FILING DATE: 2005-04-22
12 <150> PRIOR APPLICATION NUMBER: PCT/US03/33692
13 <151> PRIOR FILING DATE: 2003-10-22
15 <150> PRIOR APPLICATION NUMBER: US 60/420,129
16 <151> PRIOR FILING DATE: 2002-10-22
18 <160> NUMBER OF SEQ ID NOS: 20
20 <170> SOFTWARE: PatentIn version 3.2
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 21
24 <212> TYPE: DNA
25 <213> ORGANISM: Mycobacterium tuberculosis
27 <400> SEQUENCE: 1
28 gatataccat gggcagcagc c                                     21
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32 <211> LENGTH: 34
33 <212> TYPE: DNA
34 <213> ORGANISM: Mycobacterium tuberculosis
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41 <211> LENGTH: 35
42 <212> TYPE: DNA
43 <213> ORGANISM: Mycobacterium tuberculosis
45 <400> SEQUENCE: 3
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50 <211> LENGTH: 35
51 <212> TYPE: DNA
52 <213> ORGANISM: Mycobacterium tuberculosis
54 <400> SEQUENCE: 4
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58 <210> SEQ ID NO: 5
59 <211> LENGTH: 36
60 <212> TYPE: DNA
61 <213> ORGANISM: Mycobacterium tuberculosis

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63 <400> SEQUENCE: 5
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68 <211> LENGTH: 36
69 <212> TYPE: DNA
70 <213> ORGANISM: Mycobacterium tuberculosis
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77 <211> LENGTH: 738
78 <212> TYPE: PRT
79 <213> ORGANISM: Mycobacterium tuberculosis
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84 1 5 10 15
87 Ala Val His Arg Glu Ile Tyr Pro Lys Ala Asp Leu Ser Ile Leu Gln
88 20 25 30
91 Arg Ala Tyr Glu Val Ala Asp Gln Arg His Ala Ser Gln Leu Arg Gln
92 35 40 45
95 Ser Gly Asp Pro Tyr Ile Thr His Pro Leu Ala Val Ala Asn Ile Leu
96 50 55 60
99 Ala Glu Leu Gly Met Asp Thr Thr Thr Leu Val Ala Ala Leu Leu His
100 65 70 75 80
103 Asp Thr Val Glu Asp Thr Gly Tyr Thr Leu Glu Ala Leu Thr Glu Glu
104 85 90 95
107 Phe Gly Glu Glu Val Gly His Leu Val Asp Gly Val Thr Lys Leu Asp
108 100 105 110
111 Arg Val Val Leu Gly Ser Ala Ala Glu Gly Glu Thr Ile Arg Lys Met
112 115 120 125
115 Ile Thr Ala Met Ala Arg Asp Pro Arg Val Leu Val Ile Lys Val Ala
116 130 135 140
119 Asp Arg Leu His Asn Met Arg Thr Met Arg Phe Leu Pro Pro Glu Lys
120 145 150 155 160
123 Gln Ala Arg Lys Ala Arg Glu Thr Leu Glu Val Ile Ala Pro Leu Ala
124 165 170 175
127 His Arg Leu Gly Met Ala Ser Val Lys Trp Glu Leu Glu Asp Leu Ser
128 180 185 190
131 Phe Ala Ile Leu His Pro Lys Lys Tyr Glu Glu Ile Val Arg Leu Val
132 195 200 205
135 Ala Gly Arg Ala Pro Ser Arg Asp Thr Tyr Leu Ala Lys Val Arg Ala
136 210 215 220
139 Glu Ile Val Asn Thr Leu Thr Ala Ser Lys Ile Lys Ala Thr Val Glu
140 225 230 235 240
143 Gly Arg Pro Lys His Tyr Trp Ser Ile Tyr Gln Lys Met Ile Val Lys
144 245 250 255
147 Gly Arg Asp Phe Asp Asp Ile His Asp Leu Val Gly Val Arg Ile Leu
148 260 265 270
151 Cys Asp Glu Ile Arg Asp Cys Tyr Ala Ala Val Gly Val Val His Ser
152 275 280 285

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155 Leu Trp Gln Pro Met Ala Gly Arg Phe Lys Asp Tyr Ile Ala Gln Pro
156      290                      295                      300
159 Arg Tyr Gly Val Tyr Gln Ser Leu His Thr Thr Val Val Gly Pro Glu
160 305                      310                      315                      320
163 Gly Lys Pro Leu Glu Val Gln Ile Arg Thr Arg Asp Met His Arg Thr
164      325                      330                      335
167 Ala Glu Tyr Gly Ile Ala Ala His Trp Arg Tyr Lys Glu Ala Lys Gly
168      340                      345                      350
171 Arg Asn Gly Val Leu His Pro His Ala Ala Ala Glu Ile Asp Asp Met
172      355                      360                      365
175 Ala Trp Met Arg Gln Leu Leu Asp Trp Gln Arg Glu Ala Ala Asp Pro
176      370                      375                      380
179 Gly Glu Phe Leu Glu Ser Leu Arg Tyr Asp Leu Ala Val Gln Glu Ile
180 385                      390                      395                      400
183 Phe Val Phe Thr Pro Lys Gly Asp Val Ile Thr Leu Pro Thr Gly Ser
184      405                      410                      415
187 Thr Pro Val Asp Phe Ala Tyr Ala Val His Thr Glu Val Gly His Arg
188      420                      425                      430
191 Cys Ile Gly Ala Arg Val Asn Gly Arg Leu Val Ala Leu Glu Arg Lys
192      435                      440                      445
195 Leu Glu Asn Gly Glu Val Val Glu Val Phe Thr Ser Lys Ala Pro Asn
196      450                      455                      460
199 Ala Gly Pro Ser Arg Asp Trp Gln Gln Phe Val Val Ser Pro Arg Ala
200 465                      470                      475                      480
203 Lys Thr Lys Ile Arg Gln Trp Phe Ala Lys Glu Arg Arg Glu Glu Ala
204      485                      490                      495
207 Leu Glu Thr Gly Lys Asp Ala Met Ala Arg Glu Val Arg Arg Gly Gly
208      500                      505                      510
211 Leu Pro Leu Gln Arg Leu Val Asn Gly Glu Ser Met Ala Ala Val Ala
212      515                      520                      525
215 Arg Glu Leu His Tyr Ala Asp Val Ser Ala Leu Tyr Thr Ala Ile Gly
216      530                      535                      540
219 Glu Gly His Val Ser Ala Lys His Val Val Gln Arg Leu Leu Ala Glu
220 545                      550                      555                      560
223 Leu Gly Gly Ile Asp Gln Ala Glu Glu Glu Leu Ala Glu Arg Ser Thr
224      565                      570                      575
227 Pro Ala Thr Met Pro Arg Arg Pro Arg Ser Thr Asp Asp Val Gly Val
228      580                      585                      590
231 Ser Val Pro Gly Ala Pro Gly Val Leu Thr Lys Leu Ala Lys Cys Cys
232      595                      600                      605
235 Thr Pro Val Pro Gly Asp Val Ile Met Gly Phe Val Thr Arg Gly Gly
236      610                      615                      620
239 Gly Val Ser Val His Arg Thr Asp Cys Thr Asn Ala Ala Ser Leu Gln
240 625                      630                      635                      640
243 Gln Gln Ala Glu Arg Ile Ile Glu Val Leu Trp Ala Pro Ser Pro Ser
244      645                      650                      655
247 Ser Val Phe Leu Val Ala Ile Gln Val Glu Ala Leu Asp Arg His Arg
248      660                      665                      670
251 Leu Leu Ser Asp Val Thr Arg Ala Leu Ala Asp Glu Lys Val Asn Ile

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252          675          680          685
255 Leu Ser Ala Ser Val Thr Thr Ser Gly Asp Arg Val Ala Ile Ser Arg
256          690          695          700
259 Phe Thr Phe Glu Met Gly Asp Pro Lys His Leu Gly His Leu Leu Asn
260 705          710          715          720
263 Ala Val Arg Asn Val Glu Gly Val Tyr Asp Val Tyr Arg Val Thr Ser
264          725          730          735
267 Ala Ala
271 <210> SEQ ID NO: 8
272 <211> LENGTH: 450
273 <212> TYPE: PRT
274 <213> ORGANISM: Mycobacterium tuberculosis
276 <400> SEQUENCE: 8
278 Met Thr Ala Gln Arg Ser Thr Thr Asn Pro Val Leu Glu Pro Leu Val
279 1          5          10          15
282 Ala Val His Arg Glu Ile Tyr Pro Lys Ala Asp Leu Ser Ile Leu Gln
283          20          25          30
286 Arg Ala Tyr Glu Val Ala Asp Gln Arg His Ala Ser Gln Leu Arg Gln
287          35          40          45
290 Ser Gly Asp Pro Tyr Ile Thr His Pro Leu Ala Val Ala Asn Ile Leu
291          50          55          60
294 Ala Glu Leu Gly Met Asp Thr Thr Thr Leu Val Ala Ala Leu Leu His
295 65          70          75          80
298 Asp Thr Val Glu Asp Thr Gly Tyr Thr Leu Glu Ala Leu Thr Glu Glu
299          85          90          95
302 Phe Gly Glu Glu Val Gly His Leu Val Asp Gly Val Thr Lys Leu Asp
303          100          105          110
306 Arg Val Val Leu Gly Ser Ala Ala Glu Gly Glu Thr Ile Arg Lys Met
307          115          120          125
310 Ile Thr Ala Met Ala Arg Asp Pro Arg Val Leu Val Ile Lys Val Ala
311          130          135          140
314 Asp Arg Leu His Asn Met Arg Thr Met Arg Phe Leu Pro Pro Glu Lys
315 145          150          155          160
318 Gln Ala Arg Lys Ala Arg Glu Thr Leu Glu Val Ile Ala Pro Leu Ala
319          165          170          175
322 His Arg Leu Gly Met Ala Ser Val Lys Trp Glu Leu Glu Asp Leu Ser
323          180          185          190
326 Phe Ala Ile Leu His Pro Lys Lys Tyr Glu Glu Ile Val Arg Leu Val
327          195          200          205
330 Ala Gly Arg Ala Pro Ser Arg Asp Thr Tyr Leu Ala Lys Val Arg Ala
331          210          215          220
334 Glu Ile Val Asn Thr Leu Thr Ala Ser Lys Ile Lys Ala Thr Val Glu
335 225          230          235          240
338 Gly Arg Pro Lys His Tyr Trp Ser Ile Tyr Gln Lys Met Ile Val Lys
339          245          250          255
342 Gly Arg Asp Phe Asp Asp Ile His Asp Leu Val Gly Val Arg Ile Leu
343          260          265          270
346 Cys Asp Glu Ile Arg Asp Cys Tyr Ala Ala Val Gly Val Val His Ser
347          275          280          285

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350 Leu Trp Gln Pro Met Ala Gly Arg Phe Lys Asp Tyr Ile Ala Gln Pro
351      290                      295                      300
354 Arg Tyr Gly Val Tyr Gln Ser Leu His Thr Thr Val Val Gly Pro Glu
355 305                      310                      315                      320
358 Gly Lys Pro Leu Glu Val Gln Ile Arg Thr Arg Asp Met His Arg Thr
359                      325                      330                      335
362 Ala Glu Tyr Gly Ile Ala Ala His Trp Arg Tyr Lys Glu Ala Lys Gly
363                      340                      345                      350
366 Arg Asn Gly Val Leu His Pro His Ala Ala Ala Glu Ile Asp Asp Met
367                      355                      360                      365
370 Ala Trp Met Arg Gln Leu Leu Asp Trp Gln Arg Glu Ala Ala Asp Pro
371      370                      375                      380
374 Gly Glu Phe Leu Glu Ser Leu Arg Tyr Asp Leu Ala Val Gln Glu Ile
375 385                      390                      395                      400
378 Phe Val Phe Thr Pro Lys Gly Asp Val Ile Thr Leu Pro Thr Gly Ser
379                      405                      410                      415
382 Thr Pro Val Asp Phe Ala Tyr Ala Val His Thr Glu Val Gly His Arg
383                      420                      425                      430
386 Cys Ile Gly Ala Arg Val Asn Gly Arg Leu Val Ala Leu Glu Arg Lys
387      435                      440                      445
390 Leu Glu
391      450
394 <210> SEQ ID NO: 9
395 <211> LENGTH: 394
396 <212> TYPE: PRT
397 <213> ORGANISM: Mycobacterium tuberculosis
399 <400> SEQUENCE: 9
401 Met Thr Ala Gln Arg Ser Thr Thr Asn Pro Val Leu Glu Pro Leu Val
402 1      5      10      15
405 Ala Val His Arg Glu Ile Tyr Pro Lys Ala Asp Leu Ser Ile Leu Gln
406      20      25      30
409 Arg Ala Tyr Glu Val Ala Asp Gln Arg His Ala Ser Gln Leu Arg Gln
410      35      40      45
413 Ser Gly Asp Pro Tyr Ile Thr His Pro Leu Ala Val Ala Asn Ile Leu
414      50      55      60
417 Ala Glu Leu Gly Met Asp Thr Thr Thr Leu Val Ala Ala Leu Leu His
418 65      70      75      80
421 Asp Thr Val Glu Asp Thr Gly Tyr Thr Leu Glu Ala Leu Thr Glu Glu
422      85      90      95
425 Phe Gly Glu Glu Val Gly His Leu Val Asp Gly Val Thr Lys Leu Asp
426      100     105     110
429 Arg Val Val Leu Gly Ser Ala Ala Glu Gly Glu Thr Ile Arg Lys Met
430      115     120     125
433 Ile Thr Ala Met Ala Arg Asp Pro Arg Val Leu Val Ile Lys Val Ala
434      130     135     140
437 Asp Arg Leu His Asn Met Arg Thr Met Arg Phe Leu Pro Pro Glu Lys
438 145     150     155     160
441 Gln Ala Arg Lys Ala Arg Glu Thr Leu Glu Val Ile Ala Pro Leu Ala
442      165     170     175

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L:10 M:283 W: Missing Blank Line separator, <130> field identifier

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date